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10/686,092	10/14/2003	Karen W. Shannon	10030468-1	6820

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EXAMINER	
WHALEY, PABLO S	

ART UNIT	PAPER NUMBER
1631	

NOTIFICATION DATE	DELIVERY MODE
09/18/2008	ELECTRONIC

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

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Office Action Summary	Application No.	Applicant(s)	
	10/686,092	SHANNON, KAREN W.	
	Examiner	Art Unit	
	PABLO WHALEY	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on *20 May 2008*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-4,6-16 and 26-30* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-4, 6-16 and 26-30* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Claims Under Examination

Claims 1-4, 6-16 and 26-30 are pending. Claims 17-25 have been cancelled.

Withdrawn Rejections

The rejection of claims 1-4 and 6-16 under 35 U.S.C. 101 for non-statutory subject matter is withdrawn in view of applicant's amendments to claim 1, filed 05/20/2008.

The provisional rejection of claims 1-4, 6-16 and 26-30 for obviousness-type double patenting is withdrawn in view of applicant's arguments, filed 05/20/2008.

Claim rejections - 35 USC § 112, 2nd Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-4, 6-16 and 26-30 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims that depend directly or indirectly from claim 1 are also rejected due to said dependence.

Claims 1 and 26 (step c) recites the limitation that one or more groups of probes exhibit "substantially the same performance" across a plurality of experimental conditions, which requires that probe performance be consistent. However, claims 1 and 26 (step d) confusingly recites the "identifying"

probes by evaluating groups of candidate probes that are "not" among groups with consistent performance. For purposes of examination, this limitation is interpreted as identifying probes from groups that exhibit consistent performance.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

> This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 1, 2, 3, 6, 7, 8, 9, 14-16, 26, 27, 28, 29, and 30 are rejected under 35 U.S.C. 103(a) as being made obvious by Collins et al. (US 2004/0101846; Filed Nov. 22, 2002), in view of Lockhart et al. (US 6,344,316; Issued Feb. 5, 2002; Filed Jun. 25, 1997).

This rejection is newly applied.

Collins teaches a method and computational analysis system for identifying suitable nucleic acid sequences for use in nucleic acid arrays [Abstract, Ref. Claims 1, 15, 16]. In particular, Collins teaches steps comprising (a) identifying a plurality of candidate probe sequences for said target nucleic acid based on at least one selection criterion; (b) empirically evaluating each of said candidate probe sequences under a plurality of different experimental sets; (c) clustering said candidate probe sequences into one or more groups of candidate probe sequences based on each candidate probe sequence's collection of empirical data values, wherein each of said one or more groups exhibits substantially the same performance across said plurality of experimental sets; (d) selecting one of said one or more groups based on at least one criterion; and (e) choosing a candidate probe sequence from said selected group as said sequence of said nucleic acid that is suitable for use as a substrate immobilized probe for said target nucleic acid [Reference claim 1]. Collins also teaches selection criteria based on proximity and lack of homology [Ref. claim 2]. Collins teaches deriving a similarity matrix [Ref. Claim 7] and clustering using affinity thresholds [Ref. claim 10].

Collins does not specifically teach identifying sequences suitable for use as a substrate probes by evaluating probe sequences not among groups of candidate probe sequences that satisfy a signal intensity threshold, as in claims 1 and 26 (step d). However, this limitation would have been obvious to one of ordinary skill in the art since Collins teaches selection of the best cluster by evaluating gene expression patterns of probes including outliers [0094], selecting the best probes where a representative cluster is not identified [0096], and identifying suitable probes based on minimum performance metric including signal intensities [0097, Ref. claim 13].

Collins does not specifically teach the selection of probes suitable for use as normalization probes, as in claims 1 and 26.

Lockhart teaches normalization probes [Col. 31, lines 49-65 and Col. 32, lines 1-10] and that virtually any probe can be used as a normalization probe [Col. 31, lines 60-65]. Lockhart also teaches identifying suitable probes using thresholds [Col. 37, lines 10-30].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the probe selection method of Collin to identify probes suitable for use as normalization probes as taught by Lockhart, since Lockhart teaches that virtually any probe can be used as a normalization probe [Col. 31, lines 60-65]. One of ordinary skill in the art would have been motivated make the above modifications in order to identify probes that provide for control of variations in hybridization conditions, label intensity, and other factors that cause signal variation between arrays, as suggested by Lockhart [Col. 31, lines 49-60].

Claims 1, 2, 6-10, 12-16, and 26-30 are rejected under 35 U.S.C. 103(a) as being made obvious by Li et al. (Bioinformatics, 2001, Vol. 17, No. 11, p.1067-1076), in view of Relogio et al. (Nucleic Acids Research, 2002, Vol. 30, No. 11, p.1-10) and Ben-dor et al. (Journal of Computational Biology, 1999, Vol. 6, No. ¾, p. 281-297).

Li et al. teach a computer-implemented method and program called "ProbeSelect" for selecting an optimal number of DNA oligos for gene expression arrays. Identification and selection of candidate probes is based on selection criteria [Abstract, Fig. 2, and Table 1], frequency matching [p.1070, Col. 2, ¶ 2], free energy calculation [p.1071, Col. 1, ¶ 3], and sequence matching (and mismatching) [p.1071, Col. 1, ¶ 2], which are teachings for selection based on base composition and lack of homology. It is noted that selection of mismatch sequences is interpreted as a teaching for 'lack of homology. Selection criteria directed to frequency calculation [p.1071, Col. 1, ¶1] and free energy calculation [p.1072, Col. 1, ¶1] and [Table 4], are teachings for empirical evaluation. Candidate probes are evaluated using three different

model organisms (i.e. experimental conditions), including *E. coli* bacterial cell lines [p.1074, Col. 1, ¶1]. The "ProbeSelect" computer program as described equates to a computational analysis system [p.1069, Col. 2, ¶3]. Optimal probes are output to a user [Table 1 and 2]. Li et al. also teach subjecting arrays to experimental conditions for producing gene expression data [p.1067, Col. 2, DNA chips].

Li et al. does not specifically teach a step for empirically evaluating candidate probes, as in claims 1 and 26, step b.

Li et al. does not specifically teach limitations directed to clustering data based on gene expression, as in claims 1 and 26 (step c), and claims 13 and 26.

Li et al. does not teach deriving a similarity matrix based on expression vectors, wherein probes have similar expression patterns, as in claims 7, 8, 28, and 29.

Li et al. does not specifically teach identifying sequences suitable for use as a substrate probes by evaluating probe sequences not among groups of candidate probe sequences that satisfy a signal intensity threshold, as in claims 1 and 26 (step d).

Ben-dor teaches clustering of gene expression data obtained from the hybridization of target sequences to a microarray [Abstract, p.281-282], which shows clustering of candidate probe sequences based on empirical gene expression data. Ben-dor teaches measured expression levels of genes in variable experimental conditions [p.282, ¶3], and clustered groups exhibiting substantially the same performance across a plurality of experimental conditions [p.291, Fig. A, Fig. B, and p.293, Color Plate 2 (A), Color Plate 3], as in claims 1 and 26 (step c). Ben-dor teaches obtaining gene expression data and representing data by a real-valued expression matrix (i.e. expression vector), deriving a similarity matrix, clustering genes based on the similarity data or on the expression data [p.282, ¶3], and displaying results [p.291, Fig. A-C], as in claims 1 (step c), 7, 26 (step c, e, and f), and 28. Ben-dor teaches a clustering routine using affinity thresholds to analyze assigned and un-assigned clusters, wherein analysis stops when all data is

clustered [Fig. 2 and p.285, ¶1], which shows affinity thresholds and no further evaluation if no non-clustered probes are present, as in claims 9 and 13.

Relogio teaches a method for identifying suitable sequences of oligonucleotide probes for use as microarray probes [Abstract, p.1, Col. 2, last ¶]. In particular, Relogio teaches a probe selection algorithm where probe are excluded based on specific conditions [p.2, Col. 1, ¶2]. Relogio teaches evaluating oligonucleotide probes under different experimental conditions, and identifying optimal probes based on probe sensitivity, specificity, and dynamic range [Abstract, Fig. 1 and 2, Table 1 and 2]. Relogio also shows their methods assist in the design of DNA microarrays used for sequence analysis [Introduction, Col. 1, p.8, Discussion]. Relogio does not specifically teach evaluating any remaining probe candidates not among groups of candidate probes that satisfy a signal intensity threshold and exhibit no variation in signal, as in claims 1 and 26 (step d). However, this limitation would have been obvious to one of ordinary skill in the art since Relogio compares signal intensities for a plurality of groups of sequences with controls [Fig. 1B], identifies optimal groups of probes with signal intensity values above and below a median value (i.e. threshold) [Table 2], and analyzes groups of probes with substantially no variation in probe intensity [Table 8]. The motivation would have been to optimize the selection of oligonucleotide probes in order to improve microarray performance, as suggested by Relogio [p.1, Col. 2, last ¶].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the probe selection method of Li et al using clustering techniques taught by Ben-dor, since Ben-dor shows applications of their method specifically with microarray gene expression data [p.292, Section 4.2]. One of ordinary skill in the art would have been motivated make the above modifications in order to rapidly analyze gene expression data produced by candidate probes or to provide additional information for ensuring selection of optimal probes [Li et al., p.1076, Col. 1, ¶1].

It would further have been obvious to someone of ordinary skill in the art at the time of the instant invention to use the probe selection method taught by Relogio to identify optimal probes from the

groups of probes determined by the methods of Li and Ben-dor with the predictable expectation that only the best probes will be used to design microarrays, since Relogio teaches a method for assisting in the design of microarrays [Introduction, Col. 1, p.8, Discussion]. One of ordinary skill in the art would have been motivated to make the above modifications in order to improve microarray performance by selecting probes with optimal sensitivity and specificity, as suggested by Relogio [p.8, Discussion].

Claims 1-4, 7-9, 13-16, and 26-30 are rejected under 35 U.S.C. 103(a) as being made obvious by Sung et al. (Proceedings of the Computational Systems Bioinformatics (CSB'03), 11-14 August 2003, p.1-10), in view of Relogio et al. (Nucleic Acids Research, 2002, Vol. 30, No. 11, p.1-10) and Ben-dor et al. (Journal of Computational Biology, 1999, Vol. 6, No. ¾, p. 281-297).

Sung et al. teach a computer-implemented method for designing probes for microarrays [Abstract]. Sung shows identifying probes using a program (i.e. FindProbe), wherein three types of selection criteria are used [Section 2.1 and 2.2] including homogeneity (i.e. base content), proximity to 3' end of probes [Section 4: Sensitivity filtering], and matching and mismatching of sequences (i.e. lack of homology) [Section 5.2], as in claims 1, 2, 3, and 27. It is noted that sensitivity filtering reduced probes that form secondary structures (i.e. overlap) [Section 4], and therefore has been broadly interpreted as a teaching for minimization of candidate probes that overlap with each other, as in claim 4. Sung also shows evaluating their method of probe selection based on experimental results [Section 1.2, ¶4] and experimentally evaluating candidate probes in different experimental conditions [p.7, Section 6, Col. 1, and Table 2 and 5] as in claims 1 and 26 (step b). The "FindProbe" program is a teaching for a computational system, as in claims 14-16 and 30.

Sung et al. does not specifically teach a step for empirically evaluating candidate probes, as in claims 1 and 26, step b.

Sung et al. does not specifically teach limitations directed to clustering data based on gene expression, as in claims 1 (step c), claim 26 (step c, e, and f), and claims 13 and 26.

Sung et al. does not teach deriving a similarity matrix based on expression vectors, wherein probes have similar expression patterns, as in claims 7, 8, 28, and 29.

Sung et al. does not specifically teach identifying sequences suitable for use as a substrate probes by evaluating probe sequences not among groups of candidate probe sequences that satisfy a signal intensity threshold, as in claims 1 and 26 (step d).

Ben-dor teaches clustering of gene expression data obtained from the hybridization of target sequences to a microarray [Abstract, p.281-282], which shows clustering of candidate probe sequences based on empirical gene expression data. Ben-dor teaches measured expression levels of genes in variable experimental conditions [p.282, ¶3], and clustered groups exhibiting substantially the same performance across a plurality of experimental conditions [p.291, Fig. A, Fig. B, and p.293, Color Plate 2 (A), Color Plate 3], as in claims 1 and 26 (step c). Ben-dor teaches obtaining gene expression data and representing data by a real-valued expression matrix (i.e. expression vector), deriving a similarity matrix, clustering genes based on the similarity data or on the expression data [p.282, ¶3], and displaying results [p.291, Fig. A-C], as in claims 1 (step c), 7, 26 (step c, e, and f), and 28. Ben-dor teaches a clustering routine using affinity thresholds to analyze assigned and un-assigned clusters, wherein analysis stops when all data is clustered [Fig. 2 and p.285, ¶1], which shows no further evaluation if no non-clustered probes are present, as in claims 9 and 13.

Relogio teaches a method for identifying suitable sequences of oligonucleotide probes for use as microarray probes [Abstract, p.1, Col. 2, last ¶]. In particular, Relogio teaches a probe selection algorithm where probe are excluded based on specific conditions [p.2, Col. 1, ¶2]. Relogio teaches evaluating oligonucleotide probes under different experimental conditions, and identifying optimal probes based on probe sensitivity, specificity, and dynamic range [Abstract, Fig. 1 and 2, Table 1 and 2]. Relogio shows

their methods assist in the design of DNA microarrays used for sequence analysis [Introduction, Col. 1, p.8, Discussion]. Relogio does not specifically teach evaluating any remaining probe candidates not among groups of candidate probes that satisfy a signal intensity threshold and exhibit no variation in signal, as in claims 1 and 26 (step d). However, this limitation would have been obvious to one of ordinary skill in the art since Relogio compares signal intensities for a plurality of groups of sequences with controls [Fig. 1B], identifies optimal groups of probes with signal intensity values above and below a median value (i.e. threshold) [Table 2], and analyzes groups of probes with substantially no variation in probe intensity [Table 8]. The motivation would have been to optimize the selection of oligonucleotide probes in order to improve microarray performance, as suggested by Relogio [p.1, Col. 2, last ¶].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the probe selection method of Sung et al. using clustering techniques taught by Ben-dor, since Ben-dor shows applications of their method specifically with microarray gene expression data [p.292, Section 4.2]. One of ordinary skill in the art would have been motivated make the above modifications in order to ensure that all candidate probes produce the expected expression patterns [Ben-dor et al., Abstract] or determine which conditions that have the largest effect on clusters, as suggested by Ben-dor et al. [p.292 and 293, Section 4.2].

It would further have been obvious to someone of ordinary skill in the art at the time of the instant invention to use the probe selection method taught by Relogio to identify optimal probes from the groups of probes determined by the methods of Sung and Ben-dor with the predictable expectation that only the best probes will be used to design microarrays, since Relogio teaches a method for assisting in the design of optimal microarrays [Introduction, Col. 1, p.8, Discussion]. One of ordinary skill in the art would have been motivated to make the above modifications in order to improve microarray performance by selecting probes with optimal sensitivity and specificity, as suggested by Relogio [p.8, Discussion].

Claims 1, 10, and 11 are rejected under 35 U.S.C. 103(a) as being made obvious by Li et al. (Bioinformatics, 2001, Vol. 17, No. 11, p.1067-1076), in view of Relogio et al. (Nucleic Acids Research, 2002, Vol. 30, No. 11, p.1-10) and Ben-dor et al. (Journal of Computational Biology, 1999, Vol. 6, No. ¾, p. 281-297), as applied to claims 1, 2, 6-10, 12-16, and 26-30, above, and further in view of Cao et al. (Cross Comparison of DNA Microarray Platforms, Alliance for Cellular Signaling Laboratories, Sept. 26, 2003, p.1-23).

Li et al., Relogio, and Ben-dor et al. make obvious a method for selecting an optimal number of probes for use in gene expression arrays, as set forth above and applied to claims 1, 2, 6-10, 12-16, and 26-30.

Li et al, Relogio, and Ben-dor et al. do not specifically teach log-ratio limitation as in claims 10 and 11. However, Ben-dor et al. clearly teach and suggest the calculation of log-ratios of intensities [p.292, ¶ 1].

Cao et al. teach a method for comparing the reproducibility and sensitivity of several microarray platforms, including the Affymetrix GeneChip, custom cDNA arrays, and custom oligo arrays [Abstract]. More specifically, Cao et al. teach calculation of "log-ratio" values across a number of different experimental conditions [p.8] and values in the range of –0.16 to 0.44 [p.10], as in claims 10 and 11.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the probe selection method made obvious by Li, Relogio, and Ben-dor using log-ratio calculations taught by Cao et al., since Ben-dor et al. suggests the assessment of probes by taking the log-ratio of probe intensities [p.292, ¶ 1]. One of ordinary skill in the art would have been motivated to combine the above teachings in order to compare gene expression data for optimal probes that are

selected using different platforms [Cao et al., p.6], resulting in the practice of the instant claimed invention.

Response to Arguments

Rejection under 35 U.S.C. 103(a) over Li in view of Relogio and Ben-dor

Applicant's arguments, filed 05/20/2008, have been fully considered but are not persuasive for the following reasons.

In response to applicant's arguments against the references individually, one cannot show nonobviousness by attacking references individually where the rejections are based on combinations of references. See In re Keller, 642 F.2d 413, 208 USPQ 871 (CCPA 1981); In re Merck & Co., 800 F.2d 1091, 231 USPQ 375 (Fed. Cir. 1986).

In response to applicant's argument that Ben-dor does not teach probe selection, it is noted that Li teaches a method for selecting an optimal number of DNA oligos (i.e. probes) for gene expression arrays. Ben-dor teaches clustering of gene expression data obtained from the hybridization of target sequences to a microarray [p.281-282], which shows clustering of candidate probe sequences based on empirical gene expression data. Ben-dor also shows measured expression levels of genes in variable experimental conditions [p.282, ¶3], and clustered groups exhibiting substantially the same performance across a plurality of experimental conditions [p.291, Fig. A, Fig. B, and p.293, Color Plate 2 (A), Color Plate 3].

In response to applicant's argument that "step d" as claim requires identifying sequences of nucleic acids that are suitable as probes, it is noted that Relogio teaches a method for identifying suitable sequences of oligonucleotide probes for use as microarray probes [Abstract, p.1, Col. 2, last ¶, p.2, Col. 1, ¶2, Fig. 1 and 2, Table 1 and 2]. Relogio identifies suitable sequences through sensitivity and specificity optimization routines based on signal intensity thresholds [Fig. 2, Table 7]. Relogio identifies groups of

probe with signal intensity values above and below a median value (i.e. threshold) [Table 2], and analyzes groups of probes with substantially no variation in probe intensity [Table 8].

In response to applicant's argument that Ben-dor does not teach evaluating remaining candidate probe sequences not among said one or more groups of candidate probes, it is noted that Relogio teaches a method for identifying suitable sequences of oligonucleotide probes for use as microarray probes [Abstract, p.1, Col. 2, last ¶]. Relogio does not specifically teach evaluating any remaining probe candidates not among groups of candidate probes that satisfy a signal intensity threshold and exhibit no variation in signal, as in claims 1 and 26 (step c and d). However, this limitation would have been obvious to one of ordinary skill in the art since Relogio compares signal intensities for a plurality of groups of sequences with controls [Fig. 1B], identifies optimal groups of probes with signal intensity values above and below a median value (i.e. threshold) [Table 2], and analyzes groups of probes with substantially no variation in probe intensity [Table 8]. The motivation would have been to optimize the selection of oligonucleotide probes in order to improve microarray performance, as suggested by Relogio [p.1, Col. 2, last ¶]. For these reasons, this rejection is maintained.

Rejection under 35 U.S.C. 103(a) over Li in view of Relogio, Ben-dor, and Cao

Applicant's reiterate the above arguments, filed 05/20/2008, that Ben-dor does not teach clustering of candidate probes, and that none of the cited references teaches identifying normalization probes as required in the instant claims. Applicant's arguments have been fully considered but are not persuasive for the reasons set forth above. This rejection is maintained.

Rejection under 35 U.S.C. 103(a) over Sung in view of Relogio and Ben-dor

Applicant's reiterate the above arguments, filed 05/20/2008, that Ben-dor does not teach clustering of candidate probes, and that none of the cited references teaches identifying normalization

probes as required in the instant claims. Applicant's arguments have been fully considered but are not persuasive for the reasons set forth above. This rejection is maintained.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Pablo Whaley whose telephone number is (571)272-4425. The examiner can normally be reached on 9:30am - 6pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached at 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

/Pablo S. Whaley/

Patent Examiner

Art Unit 1631

/John S. Brusca/

Primary Examiner, Art Unit 1631